



**PATENT**  
Attorney Docket No.: **PRMG-04578**

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re Application of: Michael R. Slater, *et al.*

Serial No.: 09/641,319

Group No.:

Filed: 08/18/00

Examiner:

Entitled: **Mutant TNE Polymerases**

**CERTIFICATE RE: SEQUENCE LISTING**

Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

**CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8(a)(1)(i)(A)**

I hereby certify that this correspondence (along with any referred to as being attached or enclosed) is, on the date shown below, being deposited with the U.S. Postal Service with sufficient postage as first class mail in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

Dated: 11/12/2003

By:

*Susan M. McClintock*  
Susan M. McClintock

Sir or Madam:

I hereby state that the enclosed substitute Sequence Listing is being submitted in paper copy and on a computer-readable diskette, and that the content of the paper and computer-readable copies are the same.

Dated: 11/12/03

By:

*David A. Casimir*  
David A. Casimir  
Registration No. 42,395

MEDLEN & CARROLL, LLP  
101 Howard Street, Suite 350  
San Francisco, California 94105  
608/218-6900



## SEQUENCE LISTING

<110> Slater, Michael R.  
Huang, Fen R.  
Hartnett, James R.  
  
<120> Mutant TNE Polymerases  
  
<130> PRMG-04578  
  
<140> 09/641,319  
<141> 2000-08-18  
  
<150> 09/385,986  
<151> 1999-08-30  
  
<150> 08/484,661  
<151> 1995-06-07  
  
<160> 75  
  
<170> PatentIn version 3.2  
  
<210> 1  
<211> 2682  
<212> DNA  
<213> Thermotoga neapolitana

<220>  
<221> CDS  
<222> (1)..(2679)

<400> 1	48
atg gcg aga cta ttt ctc ttt gat ggc aca gcc ctg gcc tac agg gca	
Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala	
1 5 10 15	
tat tac gcc ctc gac aga tcc ctt tcc aca tcc aca gga att cca acg	96
Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr	
20 25 30	
aac gcc gtc tat ggc gtt gcc agg atg ctc gtt aaa ttc ata aag gaa	144
Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Phe Ile Lys Glu	
35 40 45	
cac att ata ccc gaa aag gac tac gcg gct gtg gcc ttc gac aag aag	192
His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys	
50 55 60	
gca gcg acg ttc aga cac aaa ctg ctc gaa gcg tac aag gcg caa agg	240
Ala Ala Thr Phe Arg His Lys Leu Leu Glu Ala Tyr Lys Ala Gln Arg	
65 70 75 80	
cca aag acg ccg gat ctt cta gtt cag cag cta cct tac atc aag cg	288
Pro Lys Thr Pro Asp Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg	
85 90 95	
ctg ata gaa gct ctt ggt ttc aaa gtg ctg gag ctg gaa gga tac gaa	336
Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu	
100 105 110	

gca gac gat atc atc gcc acg ctt gca gtc aag ggc tgc acg ttt ttt Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Lys Gly Cys Thr Phe Phe 115 120 125	384
gat gag att ttc ata ata acc ggt gac aag gat atg ctt caa ctt gta Asp Glu Ile Phe Ile Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val 130 135 140	432
aac gag aag ata aag gtc tgg aga atc gtc aag ggg ata tcg gat ctt Asn Glu Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu 145 150 155 160	480
gag ctt tac gat tcg aaa aag gtg aaa gaa aga tac ggt gtg gaa cca Glu Leu Tyr Asp Ser Lys Val Lys Glu Arg Tyr Gly Val Glu Pro 165 170 175	528
cat cag ata ccg gat ctt cta gca ctg acg gga gac gag ata gac aac His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Glu Ile Asp Asn 180 185 190	576
att ccc ggt gta acg gga ata ggt gaa aag acc gct gta cag ctt ctc Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu 195 200 205	624
ggc aag tac aga aat ctt gaa gac att ctg gag cat gcc cgt gaa ctc Gly Lys Tyr Arg Asn Leu Glu Asp Ile Leu Glu His Ala Arg Glu Leu 210 215 220	672
ccc cag aga gtg aga aag gct ctc ttg aga gac agg gaa gtt gcc atc Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile 225 230 235 240	720
ctc agt aaa aaa ctt gca act ctg gtg acg aac gca cct gtt gaa gtg Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val 245 250 255	768
gac tgg gaa gag atg aaa tac aga gga tac gac aag aga aaa cta ctt Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu 260 265 270	816
ccg ata ttg aaa gaa ctg gag ttt gct tcc atc atg aag gaa ctt caa Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln 275 280 285	864
ctg tac gaa gaa gca gaa ccc acc gga tac gaa atc gtg aag gat cat Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His 290 295 300	912
aag acc ttc gaa gat ctc atc gaa aag ctg aag gag gtt cca tct ttt Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe 305 310 315 320	960
gcc ctg gac ctt gaa acg tcc tcc ctt gac ccg ttc aac tgt gag ata Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile 325 330 335	1008
gtc ggc atc tcc gtg tcg ttc aaa ccg aaa aca gct tat tac att cca Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro 340 345 350	1056

ctt cat cac aga aac gcc cag aat ctt gat gaa aca ctg gtg ctg tcg Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser 355 360 365	1104
aag ttg aaa gag atc ctc gaa gac ccg tct tcg aag att gtg ggt cag Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln 370 375 380	1152
aac ctg aag tac gac tac aag gtt ctt atg gta aag ggt ata tcg cca Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro 385 390 395 400	1200
gtt tat ccg cat ttt gac acg atg ata gct gca tat ttg ctg gag cca Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro 405 410 415	1248
aac gag aaa aaa ttc aat ctc gaa gat ctg tct ttg aaa ttt ctc gga Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly 420 425 430	1296
tac aaa atg acg tct tat cag gaa ctg atg tcg ttt tcc tca cca ctt Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu 435 440 445	1344
ttt ggt ttc agc ttt gcg gat gtt ccg gta gac aag gct gcg aac tac Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr 450 455 460	1392
tcc tgc gag gat gca gac atc act tat agg ctc tac aag ata ctc agc Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser 465 470 475 480	1440
atg aag ctc cat gaa gcg gaa ctt gag aac gtc ttc tac agg ata gag Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu 485 490 495	1488
atg ccg ctt gtg aac gtt ctt gca cgc atg gaa ttg aac ggg gtg tat Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr 500 505 510	1536
gtg gac aca gaa ttc ctg aaa aag ctc tcg gag gag tac ggc aaa aag Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys 515 520 525	1584
ctc gag gaa ctg gcc gaa aaa atc tac cag ata gca gga gag ccc ttc Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe 530 535 540	1632
aac atc aat tct cca aaa cag gtt tca aag atc ctt ttt gag aag ctg Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu 545 550 555 560	1680
gga ata aaa ccc cgt gga aaa acg aca aaa aca gga gcg tac tct acc Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Ala Tyr Ser Thr 565 570 575	1728
agg ata gag gtg ttg gaa gag ata gcg aat gag cac gag ata gta ccc Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro 580 585 590	1776

ctc att ctc gag tac aga aag atc cag aaa ctg aaa tcg acc tac ata Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile 595 600 605	1824
gac acc ctt ccg aaa ctt gtg aac ccg aaa acc gga aga att cat gca Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala 610 615 620	1872
tct ttc cac cag acg ggt acc gcc act ggc agg ttg agt agc agt gat Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp 625 630 635 640	1920
cca aat ctt cag aat ctt ccg aca aag agc gaa gag gga aaa gaa att Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile 645 650 655	1968
aga aaa gcg att gtg ccc cag gat cca gac tgg tgg atc gtc agt gcg Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala 660 665 670	2016
gat tat tcc caa ata gaa ctc aga atc ctc gct cat ctc agt ggt gat Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp 675 680 685	2064
gag aac ctt gtg aag gcc ttc gag gag ggc atc gat gtg cac acc ttg Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu 690 695 700	2112
act gcc tcc agg atc tac aac gta aag cca gaa gaa gtg aac gaa gaa Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu 705 710 715 720	2160
atg cga cgg gtt gga aag atg gtg aac ttc tct ata ata tac ggt gtc Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val 725 730 735	2208
aca ccg tac ggt ctt tct gtg aga ctt gga ata ccg gtt aaa gaa gca Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala 740 745 750	2256
gaa aag atg att atc agc tat ttc aca ctg tat cca aag gtg cga agc Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser 755 760 765	2304
tac atc cag cag gtt gca gag gca aaa gag aag ggc tac gtc agg Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg 770 775 780	2352
act ctc ttt gga aga aaa aga gat att ccc cag ctc atg gca agg gac Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp 785 790 795 800	2400
aag aac acc cag tcc gaa ggc gaa aga atc gca ata aac acc ccc att Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile 805 810 815	2448
cag gga acg gcg gca gat ata ata aaa ttg gct atg ata gat ata gac Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp 820 825 830	2496

gag gag ctg aga aaa aga aac atg aaa tcc aga atg atc att cag gtt Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val 835 840 845	2544
cat gac gaa ctg gtc ttc gag gtt ccc gat gag gaa aaa gaa gaa cta His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu 850 855 860	2592
gtt gat ctg gtg aag aac aaa atg aca aat gtg gtg aaa ctc tct gtg Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val 865 870 875 880	2640
cct ctt gag gtt gac ata agc atc gga aaa agc tgg tct tga Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser 885 890	2682
<p>&lt;210&gt; 2  &lt;211&gt; 893  &lt;212&gt; PRT  &lt;213&gt; Thermotoga neapolitana</p> <p>&lt;400&gt; 2</p>	
Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala 1 5 10 15	
Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr 20 25 30	
Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu 35 40 45	
His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys 50 55 60	
Ala Ala Thr Phe Arg His Lys Leu Leu Glu Ala Tyr Lys Ala Gln Arg 65 70 75 80	
Pro Lys Thr Pro Asp Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg 85 90 95	
Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu 100 105 110	
Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Lys Gly Cys Thr Phe Phe 115 120 125	
Asp Glu Ile Phe Ile Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val 130 135 140	
Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu 145 150 155 160	

Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro  
165 170 175

His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Glu Ile Asp Asn  
180 185 190

Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu  
195 200 205

Gly Lys Tyr Arg Asn Leu Glu Asp Ile Leu Glu His Ala Arg Glu Leu  
210 215 220

Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile  
225 230 235 240

Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val  
245 250 255

Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu  
260 265 270

Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln  
275 280 285

Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His  
290 295 300

Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe  
305 310 315 320

Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile  
325 330 335

Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro  
340 345 350

Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser  
355 360 365

Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln  
370 375 380

Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro  
385 390 395 400

Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro  
405 410 415

Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly  
420 425 430

Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu  
435 440 445

Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr  
450 455 460

Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser  
465 470 475 480

Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu  
485 490 495

Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr  
500 505 510

Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys  
515 520 525

Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe  
530 535 540

Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu  
545 550 555 560

Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Ala Tyr Ser Thr  
565 570 575

Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro  
580 585 590

Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile  
595 600 605

Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala  
610 615 620

Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
625 630 635 640

Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile  
645 650 655

Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala  
660 665 670

Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp  
675 680 685

Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu  
690 695 700

Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu  
705 710 715 720

Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val  
725 730 735

Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala  
740 745 750

Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser  
755 760 765

Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg  
770 775 780

Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp  
785 790 795 800

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile  
805 810 815

Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp  
820 825 830

Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val  
835 840 845

His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Leu  
850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val  
865 870 875 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser  
885 890

```

<210> 3
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 3
catggcgaga ctatttctct ttgatggcac agccctggcc taca 44

<210> 4
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 4
aggccagggc tgtgccatca aagagaaata gtctcgc 37

<210> 5
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 5
aggccagggc tgtgccatca aagagaaata gtctcgcc 39

<210> 6
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 6
tatggcgaga ctatttctct ttgatggcac agccctggcc taca 44

<210> 7
<211> 1833
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> CDS
<222> (1)..(1830)
<223> Synthetic

```

<400> 7  
 atg aag gaa ctt caa ctg tac gaa gaa gca gaa ccc acc gga tac gaa 48  
 Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu  
 1 5 10 15  
 atc gtg aag gat cat aag acc ttc gaa gat ctc atc gaa aag ctg aag 96  
 Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys  
 20 25 30  
 gag gtt cca tct ttt gcc ctg gac ctt gaa acg tcc tcc ctt gac ccg 144  
 Glu Val Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro  
 35 40 45  
 ttc aac tgt gag ata gtc ggc atc tcc gtg tcg ttc aaa ccg aaa aca 192  
 Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr  
 50 55 60  
 gct tat tac att cca ctt cat cac aga aac gcc cag aat ctt gat gaa 240  
 Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu  
 65 70 75 80  
 aca ctg gtg ctg tcg aag ttg aaa gag atc ctc gaa gac ccg tct tcg 288  
 Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser  
 85 90 95  
 aag att gtg ggt cag aac ctg aag tac gac tac aag gtt ctt atg gta 336  
 Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val  
 100 105 110  
 aag ggt ata tcg cca gtt tat ccg cat ttt gac acg atg ata gct gca 384  
 Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala  
 115 120 125  
 tat ttg ctg gag cca aac gag aaa aaa ttc aat ctc gaa gat ctg tct 432  
 Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser  
 130 135 140  
 ttg aaa ttt ctc gga tac aaa atg acg tct tat cag gaa ctg atg tcg 480  
 Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser  
 145 150 155 160  
 ttt tcc tca cca ctt ttt ggt ttc agc ttt gcg gat gtt ccg gta gac 528  
 Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp  
 165 170 175  
 aag gct gcg aac tac tcc tgc gag gat gca gac atc act tat agg ctc 576  
 Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu  
 180 185 190  
 tac aag ata ctc agc atg aag ctc cat gaa gcg gaa ctt gag aac gtc 624  
 Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val  
 195 200 205  
 ttc tac agg ata gag atg ccg ctt gtg aac gtt ctt gca cgc atg gaa 672  
 Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu  
 210 215 220  
 ttg aac ggg gtg tat gtg gac aca gaa ttc ctg aaa aag ctc tcg gag 720  
 Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu  
 225 230 235 240

gag tac ggc aaa aag ctc gag gaa ctg gcc gaa aaa atc tac cag ata Glu Tyr Gly Lys Lys Leu Glu Leu Ala Glu Lys Ile Tyr Gln Ile 245 250 255	768
gca gga gag ccc ttc aac atc aat tct cca aaa cag gtt tca aag atc Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile 260 265 270	816
ctt ttt gag aag ctg gga ata aaa ccc cgt gga aaa acg aca aaa aca Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr 275 280 285	864
gga gcg tac tct acc agg ata gag gtg ttg gaa gag ata gcg aat gag Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Ile Ala Asn Glu 290 295 300	912
cac gag ata gta ccc ctc att ctc gag tac aga aag atc cag aaa ctg His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu 305 310 315 320	960
aaa tcg acc tac ata gac acc ctt ccg aaa ctt gtg aac ccg aaa acc Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr 325 330 335	1008
gga aga att cat gca tct ttc cac cag acg ggt acc gcc act ggc agg Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg 340 345 350	1056
ttg agt agc agt gat cca aat ctt cag aat ctt ccg aca aag agc gaa Leu Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu 355 360 365	1104
gag gga aaa gaa att aga aaa gcg att gtg ccc cag gat cca gac tgg Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp 370 375 380	1152
tgg atc gtc agt gcg gat tat tcc caa ata gaa ctc aga atc ctc gct Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala 385 390 395 400	1200
cat ctc agt ggt gat gag aac ctt gtg aag gcc ttc gag gag ggc atc His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile 405 410 415	1248
gat gtg cac acc ttg act gcc tcc agg atc tac aac gta aag cca gaa Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu 420 425 430	1296
gaa gtg aac gaa gaa atg cga cgg gtt gga aag atg gtg aac ttc tct Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser 435 440 445	1344
ata ata tac ggt gtc aca ccg tac ggt ctt tct gtg aga ctt gga ata Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile 450 455 460	1392
ccg gtt aaa gaa gca gaa aag atg att atc agc tat ttc aca ctg tat Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr 465 470 475 480	1440

cca aag gtg cga agc tac atc cag cag gtt gca gag gca aaa gag Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu 485 490 495	1488
aag ggc tac gtc agg act ctc ttt gga aga aaa aga gat att ccc cag Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln 500 505 510	1536
ctc atg gca agg gac aag aac acc cag tcc gaa ggc gaa aga atc gca Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala 515 520 525	1584
ata aac acc ccc att cag gga acg gcg gca gat ata ata aaa ttg gct Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala 530 535 540	1632
atg ata gat ata gac gag gag ctg aga aaa aga aac atg aaa tcc aga Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg 545 550 555 560	1680
atg atc att cag gtt cat gac gaa ctg gtc ttc gag gtt ccc gat gag Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu 565 570 575	1728
gaa aaa gaa gaa cta gtt gat ctg gtg aag aac aaa atg aca aat gtg Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val 580 585 590	1776
gtg aaa ctc tct gtg cct ctt gag gtt gac ata agc atc gga aaa agc Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser 595 600 605	1824
tgg tct tga Trp Ser 610	1833
<210> 8	
<211> 610	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 8	
Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu 1 5 10 15	
Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys 20 25 30	
Glu Val Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro 35 40 45	
Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr 50 55 60	

Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu  
65 70 75 80

Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser  
85 90 95

Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val  
100 105 110

Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala  
115 120 125

Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser  
130 135 140

Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser  
145 150 155 160

Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp  
165 170 175

Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu  
180 185 190

Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val  
195 200 205

Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu  
210 215 220

Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu  
225 230 235 240

Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile  
245 250 255

Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile  
260 265 270

Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr  
275 280 285

Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu  
290 295 300

His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu  
305 310 315 320

Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr  
325 330 335

Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg  
340 345 350

Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu  
355 360 365

Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp  
370 375 380

Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala  
385 390 395 400

His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile  
405 410 415

Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu  
420 425 430

Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser  
435 440 445

Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile  
450 455 460

Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr  
465 470 475 480

Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu  
485 490 495

Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln  
500 505 510

Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala  
515 520 525

Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala  
530 535 540

Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg  
545 550 555 560

Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu  
565 570 575

Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val  
580 585 590

Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser  
595 600 605

Trp Ser  
610

<210> 9  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 9  
atcgaaaagc tgaccatggc tccatctttt g

31

<210> 10  
<211> 1737  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<220>  
<221> CDS  
<222> (1)..(1734)  
<223> Synthetic

<400> 10  
atg gtt cca tct ttt gcc ctg gac ctt gaa acg tcc tcc ctt gac ccg  
Met Val Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro  
1 5 10 15

48

ttc aac tgt gag ata gtc ggc atc tcc gtg tcg ttc aaa ccg aaa aca  
Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr  
20 25 30

96

gct tat tac att cca ctt cat cac aga aac gcc cag aat ctt gat gaa  
Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu  
35 40 45

144

aca ctg gtg ctg tcg aag ttg aaa gag atc ctc gaa gac ccg tct tcg  
Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser  
50 55 60

192

aag att gtg ggt cag aac ctg aag tac gac tac aag gtt ctt atg gta  
Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val  
65 70 75 80

240

aag ggt ata tcg cca gtt tat ccg cat ttt gac acg atg ata gct gca Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala 85 90 95	288
tat ttg ctg gag cca aac gag aaa aaa ttc aat ctc gaa gat ctg tct Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser 100 105 110	336
ttg aaa ttt ctc gga tac aaa atg acg tct tat cag gaa ctg atg tcg Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser 115 120 125	384
ttt tcc tca cca ctt ttt ggt ttc agc ttt gcg gat gtt ccg gta gac Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp 130 135 140	432
aag gct gcg aac tac tcc tgc gag gat gca gac atc act tat agg ctc Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu 145 150 155 160	480
tac aag ata ctc agc atg aag ctc cat gaa gcg gaa ctt gag aac gtc Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val 165 170 175	528
ttc tac agg ata gag atg ccg ctt gtg aac gtt ctt gca cgc atg gaa Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu 180 185 190	576
ttg aac ggg gtg tat gtg gac aca gaa ttc ctg aaa aag ctc tcg gag Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu 195 200 205	624
gag tac ggc aaa aag ctc gag gaa ctg gcc gaa aaa atc tac cag ata Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile 210 215 220	672
gca gga gag ccc ttc aac atc aat tct cca aaa cag gtt tca aag atc Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile 225 230 235 240	720
ctt ttt gag aag ctg gga ata aaa ccc cgt gga aaa acg aca aaa aca Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr 245 250 255	768
gga gcg tac tct acc agg ata gag gtg ttg gaa gag ata gcg aat gag Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu 260 265 270	816
cac gag ata gta ccc ctc att ctc gag tac aga aag atc cag aaa ctg His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu 275 280 285	864
aaa tcg acc tac ata gac acc ctt ccg aaa ctt gtg aac ccg aaa acc Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr 290 295 300	912
gga aga att cat gca tct ttc cac cag acg ggt acc gcc act ggc agg Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg 305 310 315 320	960

ttg agt agc agt gat cca aat ctt cag aat ctt ccg aca aag agc gaa Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu 325 330 335	1008
gag gga aaa gaa att aga aaa gcg att gtg ccc cag gat cca gac tgg Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp 340 345 350	1056
tgg atc gtc agt gcg gat tat tcc caa ata gaa ctc aga atc ctc gct Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala 355 360 365	1104
cat ctc agt ggt gat gag aac ctt gtg aag gcc ttc gag gag ggc atc His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile 370 375 380	1152
gat gtg cac acc ttg act gcc tcc agg atc tac aac gta aag cca gaa Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu 385 390 395 400	1200
gaa gtg aac gaa gaa atg cga cgg gtt gga aag atg gtg aac ttc tct Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser 405 410 415	1248
ata ata tac ggt gtc aca ccg tac ggt ctt tct gtg aga ctt gga ata Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile 420 425 430	1296
ccg gtt aaa gaa gca gaa aag atg att atc agc tat ttc aca ctg tat Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr 435 440 445	1344
cca aag gtg cga agc tac atc cag cag gtt gca gag gca aaa gag Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu 450 455 460	1392
aag ggc tac gtc agg act ctc ttt gga aga aaa aga gat att ccc cag Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln 465 470 475 480	1440
ctc atg gca agg gac aag aac acc cag tcc gaa ggc gaa aga atc gca Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala 485 490 495	1488
ata aac acc ccc att cag gga acg gcg gca gat ata ata aaa ttg gct Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala 500 505 510	1536
atg ata gat ata gac gag gag ctg aga aaa aga aac atg aaa tcc aga Met Ile Asp Ile Asp Glu Leu Arg Lys Arg Asn Met Lys Ser Arg 515 520 525	1584
atg atc att cag gtt cat gac gaa ctg gtc ttc gag gtt ccc gat gag Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu 530 535 540	1632
gaa aaa gaa gaa cta gtt gat ctg gtg aag aac aaa atg aca aat gtg Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val 545 550 555 560	1680

gtg aaa ctc tct gtg cct ctt gag gtt gac ata agc atc gga aaa agc Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser 565 570 575	1728
tgg tct tga Trp Ser	1737
<pre> &lt;210&gt; 11 &lt;211&gt; 578 &lt;212&gt; PRT &lt;213&gt; Artificial Sequence </pre>	
<pre> &lt;220&gt; &lt;223&gt; Synthetic </pre>	
<pre> &lt;400&gt; 11 </pre>	
Met Val Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro 1 5 10 15	
Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr 20 25 30	
Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu 35 40 45	
Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser 50 55 60	
Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val 65 70 75 80	
Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala 85 90 95	
Tyr Leu Leu Glu Pro Asn Glu Lys Phe Asn Leu Glu Asp Leu Ser 100 105 110	
Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser 115 120 125	
Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp 130 135 140	
Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu 145 150 155 160	
Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val 165 170 175	

Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu  
180 185 190

Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu  
195 200 205

Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile  
210 215 220

Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile  
225 230 235 240

Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr  
245 250 255

Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu  
260 265 270

His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu  
275 280 285

Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr  
290 295 300

Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg  
305 310 315 320

Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu  
325 330 335

Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp  
340 345 350

Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala  
355 360 365

His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile  
370 375 380

Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu  
385 390 395 400

Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser  
405 410 415

Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile  
420 425 430

Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr  
435 440 445

Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu  
450 455 460

Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln  
465 470 475 480

Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala  
485 490 495

Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala  
500 505 510

Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg  
515 520 525

Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu  
530 535 540

Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val  
545 550 555 560

Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser  
565 570 575

Trp Ser

<210> 12  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 12  
tgccgtacac ctccgagagc

20

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 13  
ctcgttggc tccagcaa atgc

24

<210> 14  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 14  
tttgcctgg aacttggaaac g

21

<210> 15  
<211> 1833  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<220>  
<221> CDS  
<222> (1)..(1830)

<400> 15  
atg aag gaa ctt caa ctg tac gaa gaa gca gaa ccc acc gga tac gaa 48  
Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu  
1 5 10 15

atc gtg aag gat cat aag acc ttc gaa gat ctc atc gaa aag ctg aag 96  
Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys  
20 25 30

gag gtt cca tct ttt gcc ctg gaa ctt gaa acg tcc tcc ctt gac ccg 144  
Glu Val Pro Ser Phe Ala Leu Glu Leu Glu Thr Ser Ser Leu Asp Pro  
35 40 45

ttc aac tgt gag ata gtc ggc atc tcc gtg tcg ttc aaa ccg aaa aca 192  
Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr  
50 55 60

gct tat tac att cca ctt cat cac aga aac gcc cag aat ctt gat gaa 240  
Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu  
65 70 75 80

aca ctg gtg ctg tcg aag ttg aaa gag atc ctc gaa gac ccg tct tcg 288  
Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser  
85 90 95

aag att gtg ggt cag aac ctg aag tac gac tac aag gtt ctt atg gta Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val 100 105 110	336
aag ggt ata tcg cca gtt tat ccg cat ttt gac acg atg ata gct gca Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala 115 120 125	384
aat ttg ctg gag cca aac gag aaa aaa ttc aat ctc gaa gat ctg tct Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser 130 135 140	432
ttg aaa ttt ctc gga tac aaa atg acg tct tat cag gaa ctg atg tcg Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser 145 150 155 160	480
ttt tcc tca cca ctt ttt ggt ttc agc ttt gcg gat gtt ccg gta gac Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp 165 170 175	528
aag gct gcg aac tac tcc tgc gag gat gca gac atc act tat agg ctc Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu 180 185 190	576
tac aag ata ctc agc atg aag ctc cat gaa gcg gaa ctt gag aac gtc Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val 195 200 205	624
ttc tac agg ata gag atg ccg ctt gtg aac gtt ctt gca cgc atg gaa Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu 210 215 220	672
ttg aac ggg gtg tat gtg gac aca gaa ttc ctg aaa aag ctc tcg gag Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu 225 230 235 240	720
gag tac ggc aaa aag ctc gag gaa ctg gcc gaa aaa atc tac cag ata Glu Tyr Gly Lys Lys Leu Glu Leu Ala Glu Lys Ile Tyr Gln Ile 245 250 255	768
gca gga gag ccc ttc aac atc aat tct cca aaa cag gtt tca aag atc Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile 260 265 270	816
ctt ttt gag aag ctg gga ata aaa ccc cgt gga aaa acg aca aaa aca Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr 275 280 285	864
gga gcg tac tct acc agg ata gag gtg ttg gaa gag ata gcg aat gag Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu 290 295 300	912
cac gag ata gta ccc ctc att ctc gag tac aga aag atc cag aaa ctg His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu 305 310 315 320	960
aaa tcg acc tac ata gac acc ctt ccg aaa ctt gtg aac ccg aaa acc Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr 325 330 335	1008

gga aga att cat gca tct ttc cac cag acg ggt acc gcc act ggc agg Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg 340	345	350	1056	
ttg agt agc agt gat cca aat ctt cag aat ctt ccg aca aag agc gaa Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu 355	360	365	1104	
gag gga aaa gaa att aga aaa gcg att gtg ccc cag gat cca gac tgg Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp 370	375	380	1152	
tgg atc gtc agt gcg gat tat tcc caa ata gaa ctc aga atc ctc gct Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala 385	390	395	400	1200
cat ctc agt ggt gat gag aac ctt gtg aag gcc ttc gag gag ggc atc His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile 405	410	415	1248	
gat gtg cac acc ttg act gcc tcc agg atc tac aac gta aag cca gaa Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu 420	425	430	1296	
gaa gtg aac gaa gaa atg cga cgg gtt gga aag atg gtg aac ttc tct Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser 435	440	445	1344	
ata ata tac ggt gtc aca ccg tac ggt ctt tct gtg aga ctt gga ata Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile 450	455	460	1392	
ccg gtt aaa gaa gca gaa aag atg att atc agc tat ttc aca ctg tat Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr 465	470	475	480	1440
cca aag gtg cga agc tac atc cag cag gtt gtt gca gag gca aaa gag Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu 485	490	495	1488	
aag ggc tac gtc agg act ctc ttt gga aga aaa aga gat att ccc cag Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln 500	505	510	1536	
ctc atg gca agg gac aag aac acc cag tcc gaa ggc gaa aga atc gca Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala 515	520	525	1584	
ata aac acc ccc att cag gga acg gcg gca gat ata ata aaa ttg gct Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala 530	535	540	1632	
atg ata gat ata gac gag gag ctg aga aaa aga aac atg aaa tcc aga Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg 545	550	555	560	1680
atg atc att cag gtt cat gac gaa ctg gtc ttc gag gtt ccc gat gag Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu 565	570	575	1728	

gaa aaa gaa gaa cta gtt gat ctg gtg aag aac aaa atg aca aat gtg Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val 580 585 590	1776
gtg aaa ctc tct gtg cct ctt gag gtt gac ata agc atc gga aaa agc Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser 595 600 605	1824
tgg tct tga Trp Ser 610	1833
<210> 16 <211> 610 <212> PRT <213> Artificial Sequence	
<220> <223> Synthetic	
<400> 16	
Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu 1 5 10 15	
Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys 20 25 30	
Glu Val Pro Ser Phe Ala Leu Glu Leu Glu Thr Ser Ser Leu Asp Pro 35 40 45	
Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr 50 55 60	
Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu 65 70 75 80	
Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser 85 90 95	
Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val 100 105 110	
Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala 115 120 125	
Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser 130 135 140	
Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser 145 150 155 160	

Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp  
165 170 175

Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu  
180 185 190

Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val  
195 200 205

Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu  
210 215 220 225

Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu  
230 235 240

Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile  
245 250 255

Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile  
260 265 270

Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr  
275 280 285

Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu  
290 295 300

His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu  
305 310 315 320

Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr  
325 330 335

Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg  
340 345 350

Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu  
355 360 365

Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp  
370 375 380

Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala  
385 390 395 400

His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile  
405 410 415

Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu  
420 425 430

Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser  
435 440 445

Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile  
450 455 460

Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr  
465 470 475 480

Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu  
485 490 495

Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln  
500 505 510

Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala  
515 520 525

Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala  
530 535 540

Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg  
545 550 555 560

Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu  
565 570 575

Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val  
580 585 590

Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser  
595 600 605

Trp Ser  
610

```

<210> 17
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 17
gaccttgaca cgtcctc 17

<210> 18
<211> 1833
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> CDS
<222> (1)..(1830)

<400> 18
atg aag gaa ctt caa ctg tac gaa gaa gca gaa ccc acc gga tac gaa 48
Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu
1 5 10 15

atc gtg aag gat cat aag acc ttc gaa gat ctc atc gaa aag ctg aag 96
Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys
20 25 30

gag gtt cca tct ttt gcc ctg gac ctt gac acg tcc tcc ctt gac ccg 144
Glu Val Pro Ser Phe Ala Leu Asp Leu Asp Thr Ser Ser Leu Asp Pro
35 40 45

ttc aac tgt gag ata gtc ggc atc tcc gtg tcg ttc aaa ccg aaa aca 192
Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr
50 55 60

gct tat tac att cca ctt cat cac aga aac gcc cag aat ctt gat gaa 240
Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu
65 70 75 80

aca ctg gtg ctg tcg aag ttg aaa gag atc ctc gaa gac ccg tct tcg 288
Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser
85 90 95

aag att gtg ggt cag aac ctg aag tac gac tac aag gtt ctt atg gta 336
Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val
100 105 110

aag ggt ata tcg cca gtt tat ccg cat ttt gac acg atg ata gct gca 384
Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala
115 120 125

tat ttg ctg gag cca aac gag aaa aaa ttc aat ctc gaa gat ctg tct 432
Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser
130 135 140

```

ttg aaa ttt ctc gga tac aaa atg acg tct tat cag gaa ctg atg tcg Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser 145 150 155 160	480
ttt tcc tca cca ctt ttt ggt ttc agc ttt gcg gat gtt ccg gta gac Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp 165 170 175	528
aag gct gcg aac tac tcc tgc gag gat gca gac atc act tat agg ctc Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu 180 185 190	576
tac aag ata ctc agc atg aag ctc cat gaa gcg gaa ctt gag aac gtc Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val 195 200 205	624
ttc tac agg ata gag atg ccg ctt gtg aac gtt ctt gca cgc atg gaa Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu 210 215 220	672
ttg aac ggg gtg tat gtg gac aca gaa ttc ctg aaa aag ctc tcg gag Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu 225 230 235 240	720
gag tac ggc aaa aag ctc gag gaa ctg gcc gaa aaa atc tac cag ata Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile 245 250 255	768
gca gga gag ccc ttc aac atc aat tct cca aaa cag gtt tca aag atc Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile 260 265 270	816
ctt ttt gag aag ctg gga ata aaa ccc cgt gga aaa acg aca aaa aca Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr 275 280 285	864
gga gcg tac tct acc agg ata gag gtg ttg gaa gag ata gcg aat gag Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu 290 295 300	912
cac gag ata gta ccc ctc att ctc gag tac aga aag atc cag aaa ctg His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu 305 310 315 320	960
aaa tcg acc tac ata gac acc ctt ccg aaa ctt gtg aac ccg aaa acc Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr 325 330 335	1008
gga aga att cat gca tct ttc cac cag acg ggt acc gcc act ggc agg Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg 340 345 350	1056
ttg agt agc agt gat cca aat ctt cag aat ctt ccg aca aag agc gaa Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu 355 360 365	1104

gag gga aaa gaa att aga aaa gcg att gtg ccc cag gat cca gac tgg Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp 370 375 380	1152
tgg atc gtc agt gcg gat tat tcc caa ata gaa ctc aga atc ctc gct Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala 385 390 395 400	1200
cat ctc agt ggt gat gag aac ctt gtg aag gcc ttc gag gag ggc atc His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile 405 410 415	1248
gat gtg cac acc ttg act gcc tcc agg atc tac aac gta aag cca gaa Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu 420 425 430	1296
gaa gtg aac gaa gaa atg cga cgg gtt gga aag atg gtg aac ttc tct Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser 435 440 445	1344
ata ata tac ggt gtc aca ccg tac ggt ctt tct gtg aga ctt gga ata Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile 450 455 460	1392
ccg gtt aaa gaa gca gaa aag atg att atc agc tat ttc aca ctg tat Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr 465 470 475 480	1440
cca aag gtg cga agc tac atc cag cag gtt gtc gca gag gca aaa gag Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu 485 490 495	1488
aag ggc tac gtc agg act ctc ttt gga aga aaa aga gat att ccc cag Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln 500 505 510	1536
ctc atg gca agg gac aag aac acc cag tcc gaa ggc gaa aga atc gca Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala 515 520 525	1584
ata aac acc ccc att cag gga acg gcg gca gat ata ata aaa ttg gct Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala 530 535 540	1632
atg ata gat ata gac gag gag ctg aga aaa aga aac atg aaa tcc aga Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg 545 550 555 560	1680
atg atc att cag gtt cat gac gaa ctg gtc ttc gag gtt ccc gat gag Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu 565 570 575	1728
gaa aaa gaa gaa cta gtt gat ctg gtg aag aac aaa atg aca aat gtg Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val 580 585 590	1776

gtg aaa ctc tct gtg cct ctt gag gac ata agc atc gga aaa agc Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser 595 600 605	1824
tgg tct tga Trp Ser 610	1833
<210> 19 <211> 610 <212> PRT <213> Artificial Sequence	
<220> <223> Synthetic	
<400> 19	
Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu 1 5 10 15	
Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys 20 25 30	
Glu Val Pro Ser Phe Ala Leu Asp Leu Asp Thr Ser Ser Leu Asp Pro 35 40 45	
Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr 50 55 60	
Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu 65 70 75 80	
Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser 85 90 95	
Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val 100 105 110	
Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala 115 120 125	
Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser 130 135 140	
Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser 145 150 155 160	

Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp  
165 170 175

Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu  
180 185 190

Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val  
195 200 205

Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu  
210 215 220

Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu  
225 230 235 240

Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile  
245 250 255

Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile  
260 265 270

Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr  
275 280 285

Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu  
290 295 300

His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu  
305 310 315 320

Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr  
325 330 335

Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg  
340 345 350

Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu  
355 360 365

Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp  
370 375 380

Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala  
385 390 395 400

His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile  
405 410 415

Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu  
420 425 430

Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser  
435 440 445

Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile  
450 455 460

Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr  
465 470 475 480

Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu  
485 490 495

Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln  
500 505 510

Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala  
515 520 525

Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala  
530 535 540

Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg  
545 550 555 560

Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu  
565 570 575

Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val  
580 585 590

Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser  
595 600 605

Trp Ser  
610

<210> 20  
<211> 39  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic

<400> 20	taagtatat ctgcattc ctc gcaggagaag ttgcgcagcc	39
<210> 21		
<211> 39		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic		
<400> 21	acaaggctgc gaacttctcc tgcgaggatg cagatatca	39
<210> 22		
<211> 1833		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic		
<220>		
<221> CDS		
<222> (1)..(1830)		
<400> 22		
atg aag gaa ctt caa ctg tac gaa gaa gca gaa ccc acc gga tac gaa		48
Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu		
1 5 10 15		
atc gtg aag gat cat aag acc ttc gaa gat ctc atc gaa aag ctg aag		96
Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys		
20 25 30		
gag gtt cca tct ttt gcc ctg gac ctt gaa acg tcc tcc ctt gac ccg		144
Glu Val Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro		
35 40 45		
ttc aac tgt gag ata gtc ggc atc tcc gtg tcg ttc aaa ccg aaa aca		192
Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr		
50 55 60		
gct tat tac att cca ctt cat cac aga aac gcc cag aat ctt gat gaa		240
Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu		
65 70 75 80		
aca ctg gtg ctg tcg aag ttg aaa gag atc ctc gaa gac ccg tct tcg		288
Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser		
85 90 95		
aag att gtg ggt cag aac ctg aag tac gac tac aag gtt ctt atg gta		336
Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val		
100 105 110		
aag ggt ata tcg cca gtt tat ccg cat ttt gac acg atg ata gct gca		384
Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala		
115 120 125		

tat ttg ctg gag cca aac gag aaa aaa ttc aat ctc gaa gat ctg tct Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser 130 135 140	432
ttg aaa ttt ctc gga tac aaa atg acg tct tat cag gaa ctg atg tcg Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser 145 150 155 160	480
ttt tcc tca cca ctt ttt ggt ttc agc ttt gcg gat gtt ccg gta gac Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp 165 170 175	528
aag gct gcg aac ttc tcc tgc gag gat gca gat atc act tat agg ctc Lys Ala Ala Asn Phe Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu 180 185 190	576
tac aag ata ctc agc atg aag ctc cat gaa gcg gaa ctt gag aac gtc Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val 195 200 205	624
ttc tac agg ata gag atg ccg ctt gtg aac gtt ctt gca cgc atg gaa Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu 210 215 220	672
ttg aac ggg gtg tat gtg gac aca gaa ttc ctg aaa aag ctc tcg gag Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu 225 230 235 240	720
gag tac ggc aaa aag ctc gag gaa ctg gcc gaa aaa atc tac cag ata Glu Tyr Gly Lys Lys Leu Glu Leu Ala Glu Lys Ile Tyr Gln Ile 245 250 255	768
gca gga gag ccc ttc aac atc aat tct cca aaa cag gtt tca aag atc Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile 260 265 270	816
ctt ttt gag aag ctg gga ata aaa ccc cgt gga aaa acg aca aaa aca Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr 275 280 285	864
gga gcg tac tct acc agg ata gag gtg ttg gaa gag ata gcg aat gag Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu 290 295 300	912
cac gag ata gta ccc ctc att ctc gag tac aga aag atc cag aaa ctg His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu 305 310 315 320	960
aaa tcg acc tac ata gac acc ctt ccg aaa ctt gtg aac ccg aaa acc Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr 325 330 335	1008
gga aga att cat gca tct ttc cac cag acg ggt acc gcc act ggc agg Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg 340 345 350	1056
ttg agt agc agt gat cca aat ctt cag aat ctt ccg aca aag agc gaa Leu Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu 355 360 365	1104

gag gga aaa gaa att aga aaa gcg att gtg ccc cag gat cca gac tgg Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp 370 375 380	1152
tgg atc gtc agt gcg gat tat tcc caa ata gaa ctc aga atc ctc gct Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala 385 390 395 400	1200
cat ctc agt ggt gat gag aac ctt gtg aag gcc ttc gag gag ggc atc His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile 405 410 415	1248
gat gtg cac acc ttg act gcc tcc agg atc tac aac gta aag cca gaa Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu 420 425 430	1296
gaa gtg aac gaa gaa atg cga cgg gtt gga aag atg gtg aac ttc tct Glu Val Asn Glu Glu Met Arg Val Gly Lys Met Val Asn Phe Ser 435 440 445	1344
ata ata tac ggt gtc aca ccg tac ggt ctt tct gtg aga ctt gga ata Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile 450 455 460	1392
ccg gtt aaa gaa gca gaa aag atg att atc agc tat ttc aca ctg tat Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr 465 470 475 480	1440
cca aag gtg cga agc tac atc cag cag gtt gtt gca gag gca aaa gag Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu 485 490 495	1488
aag ggc tac gtc agg act ctc ttt gga aga aaa aga gat att ccc cag Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln 500 505 510	1536
ctc atg gca agg gac aag aac acc cag tcc gaa ggc gaa aga atc gca Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala 515 520 525	1584
ata aac acc ccc att cag gga acg gcg gca gat ata ata aaa ttg gct Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala 530 535 540	1632
atg ata gat ata gac gag gag ctg aga aaa aga aac atg aaa tcc aga Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg 545 550 555 560	1680
atg atc att cag gtt cat gac gaa ctg gtc ttc gag gtt ccc gat gag Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu 565 570 575	1728
gaa aaa gaa gaa cta gtt gat ctg gtg aag aac aaa atg aca aat gtg Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val 580 585 590	1776

gtg aaa ctc tct gtg cct ctt gag gtt gac ata agc atc gga aaa agc Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser 595	600	605	1824
tgg tct tga Trp Ser 610			1833
<p>&lt;210&gt; 23  &lt;211&gt; 610  &lt;212&gt; PRT  &lt;213&gt; Artificial Sequence</p> <p>&lt;220&gt;  &lt;223&gt; Synthetic</p> <p>&lt;400&gt; 23</p>			
<p>Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu 1 5 10 15</p>			
<p>Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys 20 25 30</p>			
<p>Glu Val Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro 35 40 45</p>			
<p>Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr 50 55 60</p>			
<p>Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu 65 70 75 80</p>			
<p>Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser 85 90 95</p>			
<p>Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val 100 105 110</p>			
<p>Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala 115 120 125</p>			
<p>Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser 130 135 140</p>			
<p>Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser 145 150 155 160</p>			
<p>Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp 165 170 175</p>			

Lys Ala Ala Asn Phe Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu  
180 185 190

Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val  
195 200 205

Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu  
210 215 220

Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu  
225 230 235 240

Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile  
245 250 255

Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile  
260 265 270

Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr  
275 280 285

Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu  
290 295 300

His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu  
305 310 315 320

Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr  
325 330 335

Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg  
340 345 350

Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu  
355 360 365

Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp  
370 375 380

Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala  
385 390 395 400

His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile  
405 410 415

Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu  
420 425 430

Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser  
435 440 445

Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile  
450 455 460

Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr  
465 470 475 480

Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu  
485 490 495

Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln  
500 505 510

Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala  
515 520 525

Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala  
530 535 540

Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg  
545 550 555 560

Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu  
565 570 575

Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val  
580 585 590

Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser  
595 600 605

Trp Ser  
610

<210> 24  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 24  
actcctgcga gaatgctgac atcacttata gg

<210> 25  
 <211> 1833  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic  
  
 <220>  
 <221> CDS  
 <222> (1)..(1830)  
  
 <400> 25

atg aag gaa ctt caa ctg tac gaa gaa gca gaa ccc acc gga tac gaa	48
Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu	
1 5 10 15	
atc gtg aag gat cat aag acc ttc gaa gat ctc atc gaa aag ctg aag	96
Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys	
20 25 30	
gag gtt cca tct ttt gcc ctg gac ctt gaa acg tcc tcc ctt gac ccg	144
Glu Val Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro	
35 40 45	
ttc aac tgt gag ata gtc ggc atc tcc gtg tcg ttc aaa ccg aaa aca	192
Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr	
50 55 60	
gct tat tac att cca ctt cat cac aga aac gcc cag aat ctt gat gaa	240
Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu	
65 70 75 80	
aca ctg gtg ctg tcg aag ttg aaa gag atc ctc gaa gac ccg tct tcg	288
Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser	
85 90 95	
aag att gtg ggt cag aac ctg aag tac gac tac aag gtt ctt atg gta	336
Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val	
100 105 110	
aag ggt ata tcg cca gtt tat ccg cat ttt gac acg atg ata gct gca	384
Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala	
115 120 125	
tat ttg ctg gag cca aac gag aaa aaa ttc aat ctc gaa gat ctg tct	432
Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser	
130 135 140	
ttg aaa ttt ctc gga tac aaa atg acg tct tat cag gaa ctg atg tcg	480
Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser	
145 150 155 160	
ttt tcc tca cca ctt ttt ggt ttc agc ttt gcg gat gtt ccg gta gac	528
Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp	
165 170 175	
aag gct gcg aac tac tcc tgc gag aat gct gac atc act tat agg ctc	576
Lys Ala Ala Asn Tyr Ser Cys Glu Asn Ala Asp Ile Thr Tyr Arg Leu	
180 185 190	

tac aag ata ctc agc atg aag ctc cat gaa gcg gaa ctt gag aac gtc Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val 195 200 205	624
ttc tac agg ata gag atg ccg ctt gtg aac gtt ctt gca cgc atg gaa Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu 210 215 220	672
ttg aac ggg gtg tat gtg gac aca gaa ttc ctg aaa aag ctc tcg gag Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu 225 230 235 240	720
gag tac ggc aaa aag ctc gag gaa ctg gcc gaa aaa atc tac cag ata Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile 245 250 255	768
gca gga gag ccc ttc aac atc aat tct cca aaa cag gtt tca aag atc Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile 260 265 270	816
ctt ttt gag aag ctg gga ata aaa ccc cgt gga aaa acg aca aaa aca Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr 275 280 285	864
gga gcg tac tct acc agg ata gag gtg ttg gaa gag ata gcg aat gag Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Ile Ala Asn Glu 290 295 300	912
cac gag ata gta ccc ctc att ctc gag tac aga aag atc cag aaa ctg His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu 305 310 315 320	960
aaa tcg acc tac ata gac acc ctt ccg aaa ctt gtg aac ccg aaa acc Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr 325 330 335	1008
gga aga att cat gca tct ttc cac cag acg ggt acc gcc act ggc agg Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg 340 345 350	1056
ttg agt agc agt gat cca aat ctt cag aat ctt ccg aca aag agc gaa Leu Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu 355 360 365	1104
gag gga aaa gaa att aga aaa gcg att gtg ccc cag gat cca gac tgg Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp 370 375 380	1152
tgg atc gtc agt gcg gat tat tcc caa ata gaa ctc aga atc ctc gct Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala 385 390 395 400	1200
cat ctc agt ggt gat gag aac ctt gtg aag gcc ttc gag gag ggc atc His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile 405 410 415	1248
gat gtg cac acc ttg act gcc tcc agg atc tac aac gta aag cca gaa Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu 420 425 430	1296

gaa gtg aac gaa gaa atg cga cgg gtt gga aag atg gtg aac ttc tct Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser 435 440 445	1344
ata ata tac ggt gtc aca ccg tac ggt ctt tct gtg aga ctt gga ata Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile 450 455 460	1392
ccg gtt aaa gaa gca gaa aag atg att atc agc tat ttc aca ctg tat Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr 465 470 475 480	1440
cca aag gtg cga agc tac atc cag cag gtt gca gag gca aaa gag Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu 485 490 495	1488
aag ggc tac gtc agg act ctc ttt gga aga aaa aga gat att ccc cag Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln 500 505 510	1536
ctc atg gca agg gac aag aac acc cag tcc gaa ggc gaa aga atc gca Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Arg Ile Ala 515 520 525	1584
ata aac acc ccc att cag gga acg gcg gca gat ata ata aaa ttg gct Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala 530 535 540	1632
atg ata gat ata gac gag gag ctg aga aaa aga aac atg aaa tcc aga Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg 545 550 555 560	1680
atg atc att cag gtt cat gac gaa ctg gtc ttc gag gtt ccc gat gag Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu 565 570 575	1728
gaa aaa gaa gaa cta gtt gat ctg gtg aag aac aaa atg aca aat gtg Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val 580 585 590	1776
gtg aaa ctc tct gtg cct ctt gag gtt gac ata agc atc gga aaa agc Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser 595 600 605	1824
tgg tct tga. Trp Ser 610	1833

<210> 26  
<211> 610  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 26

Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu  
1 5 10 15

Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys  
20 25 30

Glu Val Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro  
35 40 45

Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr  
50 55 60

Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu  
65 70 75 80

Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser  
85 90 95

Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val  
100 105 110

Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala  
115 120 125

Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser  
130 135 140

Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser  
145 150 155 160

Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp  
165 170 175

Lys Ala Ala Asn Tyr Ser Cys Glu Asn Ala Asp Ile Thr Tyr Arg Leu  
180 185 190

Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val  
195 200 205

Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu  
210 215 220

Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu  
225 230 235 240

Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile  
245 250 255

Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile  
260 265 270

Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr  
275 280 285

Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu  
290 295 300

His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu  
305 310 315 320

Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr  
325 330 335

Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg  
340 345 350

Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu  
355 360 365

Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp  
370 375 380

Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala  
385 390 395 400

His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile  
405 410 415

Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu  
420 425 430

Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser  
435 440 445

Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile  
450 455 460

Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr  
465 470 475 480

Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu  
485 490 495

Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln  
500 505 510

Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala  
515 520 525

Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala  
530 535 540

Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg  
545 550 555 560

Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu  
565 570 575

Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val  
580 585 590

Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser  
595 600 605

Trp Ser  
610

<210> 27  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 27  
tttgccttgg cccttggaaac g

21

<210> 28  
<211> 1833  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<220>  
<221> CDS  
<222> (1)..(1830)

<400> 28			
atg aag gaa ctt caa ctg tac gaa gaa gca gaa ccc acc gga tac gaa			48
Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu			
1 5 10 15			
atc gtg aag gat cat aag acc ttc gaa gat ctc atc gaa aag ctg aag			96
Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Glu Lys Leu Lys			
20 25 30			
gag gtt cca tct ttt gcc ctg gcc ctt gaa acg tcc tcc ctt gac ccg			144
Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro			
35 40 45			
ttc aac tgt gag ata gtc ggc atc tcc gtg tcg ttc aaa ccg aaa aca			192
Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr			
50 55 60			
gct tat tac att cca ctt cat cac aga aac gcc cag aat ctt gat gaa			240
Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu			
65 70 75 80			
aca ctg gtg ctg tcg aag ttg aaa gag atc ctc gaa gac ccg tct tcg			288
Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser			
85 90 95			
aag att gtg ggt cag aac ctg aag tac gac tac aag gtt ctt atg gta			336
Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val			
100 105 110			
aag ggt ata tcg cca gtt tat ccg cat ttt gac acg atg ata gct gca			384
Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala			
115 120 125			
tat ttg ctg gag cca aac gag aaa aaa ttc aat ctc gaa gat ctg tct			432
Tyr Leu Leu Glu Pro Asn Glu Lys Phe Asn Leu Glu Asp Leu Ser			
130 135 140			
ttg aaa ttt ctc gga tac aaa atg acg tct tat cag gaa ctg atg tcg			480
Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser			
145 150 155 160			
ttt tcc tca cca ctt ttt ggt ttc agc ttt gcg gat gtt ccg gta gac			528
Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp			
165 170 175			
aag gct gcg aac tac tcc tgc gag gat gca gac atc act tat agg ctc			576
Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu			
180 185 190			
tac aag ata ctc agc atg aag ctc cat gaa gcg gaa ctt gag aac gtc			624
Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val			
195 200 205			
ttc tac agg ata gag atg ccg ctt gtg aac gtt ctt gca cgc atg gaa			672
Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu			
210 215 220			

ttg aac ggg gtg tat gtg gac aca gaa ttc ctg aaa aag ctc tcg gag	720
Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu	
225 230 235 240	
gag tac ggc aaa aag ctc gag gaa ctg gcc gaa aaa atc tac cag ata	768
Glu Tyr Gly Lys Lys Leu Glu Leu Ala Glu Lys Ile Tyr Gln Ile	
245 250 255	
gca gga gag ccc ttc aac atc aat tct cca aaa cag gtt tca aag atc	816
Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile	
260 265 270	
ctt ttt gag aag ctg gga ata aaa ccc cgt gga aaa acg aca aaa aca	864
Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr	
275 280 285	
gga gcg tac tct acc agg ata gag gtg ttg gaa gag ata gcg aat gag	912
Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu	
290 295 300	
cac gag ata gta ccc ctc att ctc gag tac aga aag atc cag aaa ctg	960
His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu	
305 310 315 320	
aaa tcg acc tac ata gac acc ctt ccg aaa ctt gtg aac ccg aaa acc	1008
Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr	
325 330 335	
gga aga att cat gca tct ttc cac cag acg ggt acc gcc act ggc agg	1056
Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg	
340 345 350	
ttg agt agc agt gat cca aat ctt cag aat ctt ccg aca aag agc gaa	1104
Leu Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu	
355 360 365	
gag gga aaa gaa att aga aaa gcg att gtg ccc cag gat cca gac tgg	1152
Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp	
370 375 380	
tgg atc gtc agt gcg gat tat tcc caa ata gaa ctc aga atc ctc gct	1200
Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala	
385 390 395 400	
cat ctc agt ggt gat gag aac ctt gtg aag gcc ttc gag gag ggc atc	1248
His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile	
405 410 415	
gat gtg cac acc ttg act gcc tcc agg atc tac aac gta aag cca gaa	1296
Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu	
420 425 430	
gaa gtg aac gaa gaa atg cga cgg gtt gga aag atg gtg aac ttc tct	1344
Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser	
435 440 445	
ata ata tac ggt gtc aca ccg tac ggt ctt tct gtg aga ctt gga ata	1392
Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile	
450 455 460	

ccg gtt aaa gaa gca gaa aag atg att atc agc tat ttc aca ctg tat		1440
Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr		
465	470	475
		480
cca aag gtg cga agc tac atc cag cag gtt gtt gca gag gca aaa gag		1488
Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu		
485	490	495
aag ggc tac gtc agg act ctc ttt gga aga aaa aga gat att ccc cag		1536
Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln		
500	505	510
ctc atg gca agg gac aag aac acc cag tcc gaa ggc gaa aga atc gca		1584
Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala		
515	520	525
ata aac acc ccc att cag gga acg gcg gca gat ata ata aaa ttg gct		1632
Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala		
530	535	540
atg ata gat ata gac gag gag ctg aga aaa aga aac atg aaa tcc aga		1680
Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg		
545	550	555
560		
atg atc att cag gtt cat gac gaa ctg gtc ttc gag gtt ccc gat gag		1728
Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu		
565	570	575
gaa aaa gaa gaa cta gtt gat ctg gtg aag aac aaa atg aca aat gtg		1776
Glu Lys Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val		
580	585	590
gtg aaa ctc tct gtg cct ctt gag gtt gac ata agc atc gga aaa agc		1824
Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser		
595	600	605
tgg tct tga		1833
Trp Ser		
610		
<210> 29		
<211> 610		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> Synthetic		
<400> 29		
Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu		
1	5	10
		15
Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys		
20	25	30
Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro		
35	40	45

Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr  
50 55 60

Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu  
65 70 75 80

Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser  
85 90 95

Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val  
100 105 110

Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala  
115 120 125

Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser  
130 135 140

Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser  
145 150 155 160

Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp  
165 170 175

Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu  
180 185 190

Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val  
195 200 205

Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu  
210 215 220

Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu  
225 230 235 240

Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile  
245 250 255

Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile  
260 265 270

Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr  
275 280 285

Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu  
290 295 300

His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu  
305 310 315 320

Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr  
325 330 335

Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg  
340 345 350

Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu  
355 360 365

Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp  
370 375 380

Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala  
385 390 395 400

His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile  
405 410 415

Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu  
420 425 430

Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser  
435 440 445

Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile  
450 455 460

Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr  
465 470 475 480

Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu  
485 490 495

Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln  
500 505 510

Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala  
515 520 525

Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala  
530 535 540

Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg  
545 550 555 560

Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu  
565 570 575

Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val  
580 585 590

Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser  
595 600 605

Trp Ser  
610

<210> 30  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 30  
cctgaagtac gcgtacaagg ttcttatgg

29

<210> 31  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 31  
tcacacagga aacagctatg ac

22

<210> 32  
<211> 1833  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<220>  
<221> CDS  
<222> (1)..(1830)

<400> 32 atg aag gaa ctt caa ctg tac gaa gaa gca gaa ccc acc gga tac gaa Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu 1 5 10 15	48
atc gtg aag gat cat aag acc ttc gaa gat ctc atc gaa aag ctg aag Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys 20 25 30	96
gag gtt cca tct ttt gcc ctg gac ctt gaa acg tcc tcc ctt gac ccg Glu Val Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro 35 40 45	144
ttc aac tgt gag ata gtc ggc atc tcc gtg tcg ttc aaa ccg aaa aca Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr 50 55 60	192
gct tat tac att cca ctt cat cac aga aac gcc cag aat ctt gat gaa Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu 65 70 75 80	240
aca ctg gtg ctg tcg aag ttg aaa gag atc ctc gaa gac ccg tct tcg Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser 85 90 95	288
aag att gtg ggt cag aac ctg aag tac gcg tac aag gtt ctt atg gta Lys Ile Val Gly Gln Asn Leu Lys Tyr Ala Tyr Lys Val Leu Met Val 100 105 110	336
aag ggt ata tcg cca gtt tat ccg cat ttt gac acg atg ata gct gca Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala 115 120 125	384
tat ttg ctg gag cca aac gag aaa aaa ttc aat ctc gaa gat ctg tct Tyr Leu Leu Glu Pro Asn Glu Lys Phe Asn Leu Glu Asp Leu Ser 130 135 140	432
ttg aaa ttt ctc gga tac aaa atg acg tct tat cag gaa ctg atg tcg Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser 145 150 155 160	480
ttt tcc tca cca ctt ttt ggt ttc agc ttt gcg gat gtt ccg gta gac Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp 165 170 175	528
aag gct gcg aac tac tcc tgc gag gat gca gac atc act tat agg ctc Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu 180 185 190	576
tac aag ata ctc agc atg aag ctc cat gaa gcg gaa ctt gag aac gtc Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val 195 200 205	624
ttc tac agg ata gag atg ccg ctt gtg aac gtt ctt gca cgc atg gaa Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu 210 215 220	672
ttg aac ggg gtg tat gtg gac aca gaa ttc ctg aaa aag ctc tcg gag Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu 225 230 235 240	720

gag tac ggc aaa aag ctc gag gaa ctg gcc gaa aaa atc tac cag ata Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile 245 250 255	768
gca gga gag ccc ttc aac atc aat tct cca aaa cag gtt tca aag atc Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile 260 265 270	816
ctt ttt gag aag ctg gga ata aaa ccc cgt gga aaa acg aca aaa aca Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr 275 280 285	864
gga gcg tac tct acc agg ata gag gtg ttg gaa gag ata gcg aat gag Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Ile Ala Asn Glu 290 295 300	912
cac gag ata gta ccc ctc att ctc gag tac aga aag atc cag aaa ctg His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu 305 310 315 320	960
aaa tcg acc tac ata gac acc ctt ccg aaa ctt gtg aac ccg aaa acc Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr 325 330 335	1008
gga aga att cat gca tct ttc cac cag acg ggt acc gcc act ggc agg Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg 340 345 350	1056
ttg agt agc agt gat cca aat ctt cag aat ctt ccg aca aag agc gaa Leu Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu 355 360 365	1104
gag gga aaa gaa att aga aaa gcg att gtg ccc cag gat cca gac tgg Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp 370 375 380	1152
tgg atc gtc agt gcg gat tat tcc caa ata gaa ctc aga atc ctc gct Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala 385 390 395 400	1200
cat ctc agt ggt gat gag aac ctt gtg aag gcc ttc gag gag ggc atc His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Gly Ile 405 410 415	1248
gat gtg cac acc ttg act gcc tcc agg atc tac aac gta aag cca gaa Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu 420 425 430	1296
gaa gtg aac gaa gaa atg cga cgg gtt gga aag atg gtg aac ttc tct Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser 435 440 445	1344
ata ata tac ggt gtc aca ccg tac ggt ctt tct gtg aga ctt gga ata Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile 450 455 460	1392

ccg gtt aaa gaa gca gaa aag atg att atc agc tat ttc aca ctg tat	1440
Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr	
465 470 475 480	
cca aag gtg cga agc tac atc cag cag gtt gca gag gca aaa gag	1488
Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu	
485 490 495	
aag ggc tac gtc agg act ctc ttt gga aga aaa aga gat att ccc cag	1536
Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln	
500 505 510	
ctc atg gca agg gac aag aac acc cag tcc gaa ggc gaa aga atc gca	1584
Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala	
515 520 525	
ata aac acc ccc att cag gga acg gcg gca gat ata ata aaa ttg gct	1632
Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala	
530 535 540	
atg ata gat ata gac gag gag ctg aga aaa aga aac atg aaa tcc aga	1680
Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg	
545 550 555 560	
atg atc att cag gtt cat gac gaa ctg gtc ttc gag gtt ccc gat gag	1728
Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu	
565 570 575	
gaa aaa gaa gaa cta gtt gat ctg gtg aag aac aaa atg aca aat gtg	1776
Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val	
580 585 590	
gtg aaa ctc tct gtg cct ctt gag gtt gac ata agc atc gga aaa agc	1824
Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser	
595 600 605	
tgg tct tga	1833
Trp Ser	
610	

<210> 33  
 <211> 610  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic  
 <400> 33

Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu  
 1 5 10 15

Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys  
 20 25 30

Glu Val Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro  
 35 40 45

Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr  
50 55 60

Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu  
65 70 75 80

Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser  
85 90 95

Lys Ile Val Gly Gln Asn Leu Lys Tyr Ala Tyr Lys Val Leu Met Val  
100 105 110

Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala  
115 120 125

Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser  
130 135 140

Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser  
145 150 155 160

Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp  
165 170 175

Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu  
180 185 190

Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val  
195 200 205

Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu  
210 215 220

Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu  
225 230 235 240

Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile  
245 250 255

Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile  
260 265 270

Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr  
275 280 285

Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu  
290 295 300

His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu  
305 310 315 320

Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr  
325 330 335

Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg  
340 345 350

Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu  
355 360 365

Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp  
370 375 380

Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala  
385 390 395 400

His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile  
405 410 415

Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu  
420 425 430

Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser  
435 440 445

Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile  
450 455 460

Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr  
465 470 475 480

Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu  
485 490 495

Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln  
500 505 510

Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala  
515 520 525

Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala  
530 535 540

Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg  
545 550 555 560

Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu  
565 570 575

Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val  
580 585 590

Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser  
595 600 605

Trp Ser  
610

<210> 34  
<211> 1833  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<220>  
<221> CDS  
<222> (1)..(1830)

<400> 34  
atg aag gaa ctt caa ctg tac gaa gaa gca gaa ccc acc gga tac gaa 48  
Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu  
1 5 10 15

atc gtg aag gat cat aag acc ttc gaa gat ctc atc gaa aag ctg aag 96  
Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys  
20 25 30

gag gtt cca tct ttt gcc ctg gcc ctt gaa acg tcc tcc ctt gac ccg 144  
Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro  
35 40 45

ttc aac tgt gag ata gtc ggc atc tcc gtg tcg ttc aaa ccg aaa aca 192  
Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr  
50 55 60

gct tat tac att cca ctt cat cac aga aac gcc cag aat ctt gat gaa 240  
Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu  
65 70 75 80

aca ctg gtg ctg tcg aag ttg aaa gag atc ctc gaa gac ccg tct tcg 288  
Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser  
85 90 95

aag att gtg ggt cag aac ctg aag tac gcg tac aag gtt ctt atg gta 336  
Lys Ile Val Gly Gln Asn Leu Lys Tyr Ala Tyr Lys Val Leu Met Val  
100 105 110

aag ggt ata tcg cca gtt tat ccg cat ttt gac acg atg ata gct gca Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala 115 120 125	384
tat ttg ctg gag cca aac gag aaa aaa ttc aat ctc gaa gat ctg tct Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser 130 135 140	432
ttg aaa ttt ctc gga tac aaa atg acg tct tat cag gaa ctg atg tcg Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser 145 150 155 160	480
ttt tcc tca cca ctt ttt ggt ttc agc ttt gcg gat gtt ccg gta gac Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp 165 170 175	528
aag gct gcg aac tac tcc tgc gag gat gca gac atc act tat agg ctc Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu 180 185 190	576
tac aag ata ctc agc atg aag ctc cat gaa gcg gaa ctt gag aac gtc Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val 195 200 205	624
ttc tac agg ata gag atg ccg ctt gtg aac gtt ctt gca cgc atg gaa Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu 210 215 220	672
ttg aac ggg gtg tat gtg gac aca gaa ttc ctg aaa aag ctc tcg gag Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu 225 230 235 240	720
gag tac ggc aaa aag ctc gag gaa ctg gcc gaa aaa atc tac cag ata Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile 245 250 255	768
gca gga gag ccc ttc aac atc aat tct cca aaa cag gtt tca aag atc Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile 260 265 270	816
ctt ttt gag aag ctg gga ata aaa ccc cgt gga aaa acg aca aaa aca Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr 275 280 285	864
gga gcg tac tct acc agg ata gag gtg ttg gaa gag ata gcg aat gag Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu 290 295 300	912
cac gag ata gta ccc ctc att ctc gag tac aga aag atc cag aaa ctg His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu 305 310 315 320	960
aaa tcg acc tac ata gac acc ctt ccg aaa ctt gtg aac ccg aaa acc Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr 325 330 335	1008
gga aga att cat gca tct ttc cac cag acg ggt acc gcc act ggc agg Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg 340 345 350	1056

ttg agt agc agt gat cca aat ctt cag aat ctt ccg aca aag agc gaa Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu 355	360	365	1104	
gag gga aaa gaa att aga aaa gcg att gtg ccc cag gat cca gac tgg Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp 370	375	380	1152	
tgg atc gtc agt gcg gat tat tcc caa ata gaa ctc aga atc ctc gct Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala 385	390	395	400	1200
cat ctc agt ggt gat gag aac ctt gtg aag gcc ttc gag gag ggc atc His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile 405	410	415	1248	
gat gtg cac acc ttg act gcc tcc agg atc tac aac gta aag cca gaa Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu 420	425	430	1296	
gaa gtg aac gaa gaa atg cga cgg gtt gga aag atg gtg aac ttc tct Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser 435	440	445	1344	
ata ata tac ggt gtc aca ccg tac ggt ctt tct gtg aga ctt gga ata Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile 450	455	460	1392	
ccg gtt aaa gaa gca gaa aag atg att atc agc tat ttc aca ctg tat Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr 465	470	475	480	1440
cca aag gtg cga agc tac atc cag cag gtt gtt gca gag gca aaa gag Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu 485	490	495	1488	
aag ggc tac gtc agg act ctc ttt gga aga aaa aga gat att ccc cag Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln 500	505	510	1536	
ctc atg gca agg gac aag aac acc cag tcc gaa ggc gaa aga atc gca Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala 515	520	525	1584	
ata aac acc ccc att cag gga acg gcg gca gat ata ata aaa ttg gct Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala 530	535	540	1632	
atg ata gat ata gac gag gag ctg aga aaa aga aac atg aaa tcc aga Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg 545	550	555	560	1680
atg atc att cag gtt cat gac gaa ctg gtc ttc gag gtt ccc gat gag Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu 565	570	575	1728	
gaa aaa gaa gaa cta gtt gat ctg gtg aag aac aaa atg aca aat gtg Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val 580	585	590	1776	

gtg aaa ctc tct gtg cct ctt gag gac ata agc atc gga aaa agc Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser 595 600 605	1824
tgg tct tga Trp Ser 610	1833
<210> 35 <211> 610 <212> PRT <213> Artificial Sequence	
<220> <223> Synthetic	
<400> 35	
Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu 1 5 10 15	
Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys 20 25 30	
Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro 35 40 45	
Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr 50 55 60	
Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu 65 70 75 80	
Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser 85 90 95	
Lys Ile Val Gly Gln Asn Leu Lys Tyr Ala Tyr Lys Val Leu Met Val 100 105 110	
Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala 115 120 125	
Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser 130 135 140	
Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser 145 150 155 160	
Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp 165 170 175	

Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu  
180 185 190

Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val  
195 200 205

Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu  
210 215 220

Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu  
225 230 235 240

Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile  
245 250 255

Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile  
260 265 270

Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr  
275 280 285

Gly Ala Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu  
290 295 300

His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu  
305 310 315 320

Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr  
325 330 335

Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg  
340 345 350

Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu  
355 360 365

Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp  
370 375 380

Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala  
385 390 395 400

His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile  
405 410 415

Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu  
420 425 430

Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser  
435 440 445

Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile  
450 455 460

Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr  
465 470 475 480

Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu  
485 490 495

Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln  
500 505 510

Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala  
515 520 525

Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala  
530 535 540

Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg  
545 550 555 560

Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu  
565 570 575

Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val  
580 585 590

Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser  
595 600 605

Trp Ser  
610

<210> 36  
<211> 1716  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<220>  
<221> CDS  
<222> (1) .. (1713)

<400> 36  
 atg ctt gaa acg tcc tcc ctt gac ccg ttc aac tgt gag ata gtc ggc 48  
 Met Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile Val Gly  
 1 5 10 15  
 atc tcc gtg tcg ttc aaa ccg aaa aca gct tat tac att cca ctt cat 96  
 Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro Leu His  
 20 25 30  
 cac aga aac gcc cag aat ctt gat gaa aca ctg gtg ctg tcg aag ttg 144  
 His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser Lys Leu  
 35 40 45  
 aaa gag atc ctc gaa gac ccg tct tcg aag att gtg ggt cag aac ctg 192  
 Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln Asn Leu  
 50 55 60  
 aag tac gac tac aag gtt ctt atg gta aag ggt ata tcg cca gtt tat 240  
 Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro Val Tyr  
 65 70 75 80  
 ccg cat ttt gac acg atg ata gct gca tat ttg ctg gag cca aac gag 288  
 Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro Asn Glu  
 85 90 95  
 aaa aaa ttc aat ctc gaa gat ctg tct ttg aaa ttt ctc gga tac aaa 336  
 Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly Tyr Lys  
 100 105 110  
 atg acg tct tat cag gaa ctg atg tcg ttt tcc tca cca ctt ttt ggt 384  
 Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu Phe Gly  
 115 120 125  
 ttc agc ttt gcg gat gtt ccg gta gac aag gct gcg aac tac tcc tgc 432  
 Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr Ser Cys  
 130 135 140  
 gag gat gca gac atc act tat agg ctc tac aag ata ctc agc atg aag 480  
 Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser Met Lys  
 145 150 155 160  
 ctc cat gaa gcg gaa ctt gag aac gtc ttc tac agg ata gag atg ccg 528  
 Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu Met Pro  
 165 170 175  
 ctt gtg aac gtt ctt gca cgc atg gaa ttg aac ggg gtg tat gtg gac 576  
 Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr Val Asp  
 180 185 190  
 aca gaa ttc ctg aaa aag ctc tcg gag gag tac ggc aaa aag ctc gag 624  
 Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys Leu Glu  
 195 200 205  
 gaa ctg gcc gaa aaa atc tac cag ata gca gga gag ccc ttc aac atc 672  
 Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe Asn Ile  
 210 215 220  
 aat tct cca aaa cag gtt tca aag atc ctt ttt gag aag ctg gga ata 720  
 Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu Gly Ile  
 225 230 235 240

aaa ccc cgt gga aaa acg aca aaa aca gga gcg tac tct acc agg ata Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Ala Tyr Ser Thr Arg Ile 245 250 255	768
gag gtg ttg gaa gag ata gcg aat gag cac gag ata gta ccc ctc att Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro Leu Ile 260 265 270	816
ctc gag tac aga aag atc cag aaa ctg aaa tcg acc tac ata gac acc Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile Asp Thr 275 280 285	864
ctt ccg aaa ctt gtg aac ccg aaa acc gga aga att cat gca tct ttc Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala Ser Phe 290 295 300	912
cac cag acg ggt acc gcc act ggc agg ttg agt agc agt gat cca aat His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn 305 310 315 320	960
ctt cag aat ctt ccg aca aag agc gaa gag gga aaa gaa att aga aaa Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile Arg Lys 325 330 335	1008
gcg att gtg ccc cag gat cca gac tgg tgg atc gtc agt gcg gat tat Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala Asp Tyr 340 345 350	1056
tcc caa ata gaa ctc aga atc ctc gct cat ctc agt ggt gat gag aac Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp Glu Asn 355 360 365	1104
ctt gtg aag gcc ttc gag gag ggc atc gat gtg cac acc ttg act gcc Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu Thr Ala 370 375 380	1152
tcc agg atc tac aac gta aag cca gaa gaa gtg aac gaa gaa atg cga Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu Met Arg 385 390 395 400	1200
cgg gtt gga aag atg gtg aac ttc tct ata ata tac ggt gtc aca ccg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val Thr Pro 405 410 415	1248
tac ggt ctt tct gtg aga ctt gga ata ccg gtt aaa gaa gca gaa aag Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala Glu Lys 420 425 430	1296
atg att atc agc tat ttc aca ctg tat cca aag gtg cga agc tac atc Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser Tyr Ile 435 440 445	1344
cag cag gtt gca gag gca aaa gag aag ggc tac gtc agg act ctc Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg Thr Leu 450 455 460	1392
ttt gga aga aaa aga gat att ccc cag ctc atg gca agg gac aag aac Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp Lys Asn 465 470 475 480	1440

acc cag tcc gaa ggc gaa aga atc gca ata aac acc ccc att cag gga Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile Gln Gly 485 490 495	1488
acg gcg gca gat ata ata aaa ttg gct atg ata gat ata gac gag gag Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp Glu Glu 500 505 510	1536
ctg aga aaa aga aac atg aaa tcc aga atg atc att cag gtt cat gac Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val His Asp 515 520 525	1584
gaa ctg gtc ttc gag gtt ccc gat gag gaa aaa gaa gaa cta gtt gat Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu Val Asp 530 535 540	1632
ctg gtg aag aac aaa atg aca aat gtg gtg aaa ctc tct gtg cct ctt Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val Pro Leu 545 550 555 560	1680
gag gtt gac ata agc atc gga aaa agc tgg tct tga Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser 565 570	1716
<p>&lt;210&gt; 37  &lt;211&gt; 571  &lt;212&gt; PRT  &lt;213&gt; Artificial Sequence</p> <p>&lt;220&gt;  &lt;223&gt; Synthetic</p> <p>&lt;400&gt; 37</p>	
Met Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile Val Gly 1 5 10 15	
Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro Leu His 20 25 30	
His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser Lys Leu 35 40 45	
Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln Asn Leu 50 55 60	
Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro Val Tyr 65 70 75 80	
Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro Asn Glu 85 90 95	
Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly Tyr Lys 100 105 110	

Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu Phe Gly  
115 120 125

Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr Ser Cys  
130 135 140

Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser Met Lys  
145 150 155 160

Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu Met Pro  
165 170 175

Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr Val Asp  
180 185 190

Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys Leu Glu  
195 200 205

Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe Asn Ile  
210 215 220

Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu Gly Ile  
225 230 235 240

Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Ala Tyr Ser Thr Arg Ile  
245 250 255

Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro Leu Ile  
260 265 270

Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile Asp Thr  
275 280 285

Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala Ser Phe  
290 295 300

His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn  
305 310 315 320

Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile Arg Lys  
325 330 335

Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala Asp Tyr  
340 345 350

Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp Glu Asn  
355 360 365

Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu Thr Ala  
 370 375 380  
 Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu Met Arg  
 385 390 395 400  
 Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val Thr Pro  
 405 410 415  
 Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala Glu Lys  
 420 425 430  
 Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser Tyr Ile  
 435 440 445  
 Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg Thr Leu  
 450 455 460  
 Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp Lys Asn  
 465 470 475 480  
 Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile Gln Gly  
 485 490 495  
 Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp Glu Glu  
 500 505 510  
 Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val His Asp  
 515 520 525  
 Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu Val Asp  
 530 535 540  
 Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val Pro Leu  
 545 550 555 560  
 Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser  
 565 570  
  
 <210> 38  
 <211> 1485  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic

<220>  
 <221> CDS  
 <222> (1)...(1482)

<400> 38 atg aag gaa ctt caa ctg tac gaa gaa gca gaa ccc acc gga tac gaa Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu 1 5 10 15	48
atc gtg aag gat cat aag acc ttc gaa gat ctg tot ttg aaa ttt ctc Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ser Leu Lys Phe Leu 20 25 30	96
gga tac aaa atg acg tct tat cag gaa ctg atg tcg ttt tcc tca cca Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro 35 40 45	144
ctt ttt ggt ttc agc ttt gcg gat gtt ccg gta gac aag gct gcg aac Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn 50 55 60	192
tac tcc tgc gag gat gca gac atc act tat agg ctc tac aag ata ctc Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu 65 70 75 80	240
agc atg aag ctc cat gaa gcg gaa ctt gag aac gtc ttc tac agg ata Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile 85 90 95	288
gag atg ccg ctt gtg aac gtt ctt gca cgc atg gaa ttg aac ggg gtg Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val 100 105 110	336
tat gtg gac aca gaa ttc ctg aaa aag ctc tcg gag gag tac ggc aaa Tyr Val Asp Thr Glu Phe Leu Lys Leu Ser Glu Glu Tyr Gly Lys 115 120 125	384
aag ctc gag gaa ctg gcc gaa aaa atc tac cag ata gca gga gag ccc Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro 130 135 140	432
ttc aac atc aat tct cca aaa cag gtt tca aag atc ctt ttt gag aag Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys 145 150 155 160	480
ctg gga ata aaa ccc cgt gga aaa acg aca aaa aca gga gcg tac tct Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Ala Tyr Ser 165 170 175	528
acc agg ata gag gtg ttg gaa gag ata gcg aat gag cac gag ata gta Thr Arg Ile Glu Val Leu Glu Ile Ala Asn Glu His Glu Ile Val 180 185 190	576
ccc ctc att ctc gag tac aga aag atc cag aaa ctg aaa tcg acc tac Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr 195 200 205	624
ata gac acc ctt ccg aaa ctt gtg aac ccg aaa acc gga aga att cat Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His 210 215 220	672

gca tct ttc cac cag acg ggt acc gcc act ggc agg ttg agt agc agt Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser 225 230 235 240	720
gat cca aat ctt cag aat ctt ccg aca aag agc gaa gag gga aaa gaa Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu 245 250 255	768
att aga aaa gcg att gtg ccc cag gat cca gac tgg tgg atc gtc agt Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser 260 265 270	816
gcg gat tat tcc caa ata gaa ctc aga atc ctc gct cat ctc agt ggt Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly 275 280 285	864
gat gag aac ctt gtg aag gcc ttc gag gag ggc atc gat gtg cac acc Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr 290 295 300	912
ttg act gcc tcc agg atc tac aac gta aag cca gaa gaa gtg aac gaa Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu 305 310 315 320	960
gaa atg cga cgg gtt gga aag atg gtg aac ttc tct ata ata tac ggt Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly 325 330 335	1008
gtc aca ccg tac ggt ctt tct gtg aga ctt gga ata ccg gtt aaa gaa Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu 340 345 350	1056
gca gaa aag atg att atc agc tat ttc aca ctg tat cca aag gtg cga Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg 355 360 365	1104
agc tac atc cag cag gtt gtt gca gag gca aaa gag aag ggc tac gtc Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val 370 375 380	1152
agg act ctc ttt gga aga aaa aga gat att ccc cag ctc atg gca agg Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg 385 390 395 400	1200
gac aag aac acc cag tcc gaa ggc gaa aga atc gca ata aac acc ccc Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro 405 410 415	1248
att cag gga acg gcg gca gat ata ata aaa ttg gct atg ata gat ata Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile 420 425 430	1296
gac gag gag ctg aga aaa aga aac atg aaa tcc aga atg atc att cag Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln 435 440 445	1344
gtt cat gac gaa ctg gtc ttc gag gtt ccc gat gag gaa aaa gaa gaa Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu 450 455 460	1392

cta gtt gat ctg gtg aag aac aaa atg aca aat gtg gtg aaa ctc tct	1440
Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser	
465 470 475 480	
gtg cct ctt gag gtt gac ata agc atc gga aaa agc tgg tct tga	1485
Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser	
485 490	
<210> 39	
<211> 494	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 39	
Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu	
1 5 10 15	
Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ser Leu Lys Phe Leu	
20 25 30	
Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro	
35 40 45	
Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn	
50 55 60	
Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu	
65 70 75 80	
Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile	
85 90 95	
Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val	
100 105 110	
Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys	
115 120 125	
Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro	
130 135 140	
Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys	
145 150 155 160	
Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Ala Tyr Ser	
165 170 175	

Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val  
180 185 190

Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr  
195 200 205

Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His  
210 215 220

Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser  
225 230 235 240

Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu  
245 250 255

Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser  
260 265 270

Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly  
275 280 285

Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr  
290 295 300

Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu  
305 310 315 320

Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly  
325 330 335

Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu  
340 345 350

Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg  
355 360 365

Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val  
370 375 380

Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg  
385 390 395 400

Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro  
405 410 415

Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile  
420 425 430

Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln  
435 440 445

Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu  
450 455 460

Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser  
465 470 475 480

Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser  
485 490

<210> 40  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 40  
cgccagggtt ttcccagtca cgac

24

<210> 41  
<211> 74  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 41  
ataagcgcca ttgatgttcc tctctactcg aaagtttagag aggacacaccc cgatccatat 60  
agtgagtcgt atta 74

<210> 42  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 42  
taatacgact cactataggg cgaat

25

<210> 43  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 43	25
gaatcgctgt atgcagtgaa aactc	
<210> 44	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 44	25
cttgattgac aaggatggat ggcta	
<210> 45	
<211> 33	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 45	33
catggtttaa atcctgtgt aaattgttat ccg	
<210> 46	
<211> 29	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 46	29
cggataacaa tttcacacag gatttaaac	
<210> 47	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 47	25
taatacgact cactataggg cgaat	
<210> 48	
<211> 31	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 48	31
catgccatgg catgcattta cgttgacacc a	

```

<210> 49
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 49
tcccccggt tgcgctcact gcccgcttc cagt 34

<210> 50
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 50
agtttatcga tggcactttt cggggaaatg tgcg 34

<210> 51
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 51
agtttatcga taagcgatgc cgggagcaga caagc 35

<210> 52
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 52
Glu Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val
1 5 10 15

Tyr

```

<210> 53  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 53

Thr Arg Gln Ile Val Leu Asp Thr Glu Thr Thr Gly Met Asn Gln Ile  
1 5 10 15

Gly

<210> 54  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 54

Arg Val Ile Tyr Met Pro Phe Asp Asn Glu Arg Asp Met Leu Met Glu  
1 5 10 15

Tyr Ile

<210> 55  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 55

Met Ile Val Ser Asp Ile Glu Ala Asn Ala Leu Leu Glu Ser Val  
1 5 10 15

<210> 56  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 56

Lys Ala Pro Val Phe Ala Phe Asp Thr Glu Thr Asp Ser Leu Asp Asn  
1 5 10 15

Ile Ser

<210> 57  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 57

Glu Ser Pro Ser Phe Ala Ile Asp Leu Glu Thr Ser Ser Leu Asp Pro  
1 5 10 15

Phe Asp

<210> 58  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 58

Glu Val Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro  
1 5 10 15

Phe Asn

<210> 59  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 59

Leu Val Ala His Asn Ala Ser Phe Asp Met Gly Phe Leu Asn  
1 5 10

<210> 60  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 60

Leu Val Ile His Asn Ala Ala Phe Asp Ile Gly Phe Met Asp  
1 5 10

<210> 61  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 61

Phe Thr Gly Trp Asn Ile Glu Gly Phe Asp Val Pro Tyr Ile Met  
1 5 10 15

<210> 62  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 62

Val Phe His Asn Gly His Lys Tyr Asp Val Pro Ala Leu Thr  
1 5 10

<210> 63  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 63

Val Gly Gln Asn Leu Lys Tyr Asp Arg Gly Ile Leu Ala  
1 5 10

<210> 64  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 64

Val Gly Gln Asn Leu Lys Phe Asp Tyr Lys Val Leu Met  
1 5 10

<210> 65  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 65

Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met  
1 5 10

<210> 66  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 66

Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln His  
1 5 10

<210> 67  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 67

Ala Leu Cys Ala Arg Tyr Glu Ile Asp Asn Ser Lys Arg  
1 5 10

<210> 68  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 68

Asp Lys Ile Arg Gly Phe Ile Asp Leu Val Leu Ser  
1 5 10

<210> 69  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 69

Glu Glu Met Met Asp Tyr Asn Val Gln Asp Val Val Val Thr  
1 5 10

<210> 70  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 70

Glu Glu Ala Gly Arg Tyr Ala Ala Glu Asp Ala Asp Val Thr  
1 5 10

<210> 71  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 71

Glu Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr  
1 5 10

<210> 72  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 72

Asp Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr  
1 5 10

<210> 73  
<211> 928  
<212> PRT  
<213> Escherichia coli

<400> 73

Met Val Gln Ile Pro Gln Asn Pro Leu Ile Leu Val Asp Gly Ser Ser  
1 5 10 15

Tyr Leu Tyr Arg Ala Tyr His Ala Phe Pro Pro Leu Thr Asn Ser Ala  
20 25 30

Gly Glu Pro Thr Gly Ala Met Tyr Gly Val Leu Asn Met Leu Arg Ser  
35 40 45

Leu Ile Met Gln Tyr Lys Pro Thr His Ala Ala Val Val Phe Asp Ala  
50 55 60

Lys Gly Lys Thr Phe Arg Asp Glu Leu Phe Glu His Tyr Lys Ser His  
65 70 75 80

Arg Pro Pro Met Pro Asp Asp Leu Arg Ala Gln Ile Glu Pro Leu His  
85 90 95

Ala Met Val Lys Ala Met Gly Leu Pro Leu Leu Ala Val Ser Gly Val  
100 105 110

Glu Ala Asp Asp Val Ile Gly Thr Leu Ala Arg Glu Ala Glu Lys Ala  
115 120 125

Gly Arg Pro Val Leu Ile Ser Thr Gly Asp Lys Asp Met Ala Gln Leu  
130 135 140

Val Thr Pro Asn Ile Thr Leu Ile Asn Thr Met Thr Asn Thr Ile Leu  
145 150 155 160

Gly Pro Glu Glu Val Val Asn Lys Tyr Gly Val Pro Pro Glu Leu Ile  
165 170 175

Ile Asp Phe Leu Ala Leu Met Gly Asp Ser Ser Asp Asn Ile Pro Gly  
180 185 190

Val Pro Gly Val Gly Glu Lys Thr Ala Gln Ala Leu Leu Gln Gly Leu  
195 200 205

Gly Gly Leu Asp Thr Leu Tyr Ala Glu Pro Glu Lys Ile Ala Gly Leu  
210 215 220

Ser Phe Arg Gly Ala Lys Thr Met Ala Ala Lys Leu Glu Gln Asn Lys  
225 230 235 240

Glu Val Ala Tyr Leu Ser Tyr Gln Leu Ala Thr Ile Lys Thr Asp Val  
245 250 255

Glu Leu Glu Leu Thr Cys Glu Gln Leu Glu Val Gln Gln Pro Ala Ala  
260 265 270

Glu Glu Leu Leu Gly Leu Phe Lys Lys Tyr Glu Phe Lys Arg Trp Thr  
275 280 285

Ala Asp Val Glu Ala Gly Lys Trp Leu Gln Ala Lys Gly Ala Lys Pro  
290 295 300

Ala Ala Lys Pro Gln Glu Thr Ser Val Ala Asp Glu Ala Pro Glu Val  
305 310 315 320

Thr Ala Thr Val Ile Ser Tyr Asp Asn Tyr Val Thr Ile Leu Asp Glu  
325 330 335

Glu Thr Leu Lys Ala Trp Ile Ala Lys Leu Glu Lys Ala Pro Val Phe  
340 345 350

Ala Phe Asp Thr Glu Thr Asp Ser Leu Asp Asn Ile Ser Ala Asn Leu  
355 360 365

Val Gly Leu Ser Phe Ala Ile Glu Pro Gly Val Ala Ala Tyr Ile Pro  
370 375 380

Val Ala His Asp Tyr Leu Asp Ala Pro Asp Gln Ile Ser Arg Glu Arg  
385 390 395 400

Ala Leu Glu Leu Leu Lys Pro Leu Leu Glu Asp Glu Lys Ala Leu Lys  
405 410 415

Val Gly Gln Asn Leu Lys Tyr Asp Arg Gly Ile Leu Ala Asn Tyr Gly  
420 425 430

Ile Glu Leu Arg Gly Ile Ala Phe Asp Thr Met Leu Glu Ser Tyr Ile  
435 440 445

Leu Asn Ser Val Ala Gly Arg His Asp Met Asp Ser Leu Ala Glu Arg  
450 455 460

Trp Leu Lys His Lys Thr Ile Thr Phe Glu Glu Ile Ala Gly Lys Gly  
465 470 475 480

Lys Asn Gln Leu Thr Phe Asn Gln Ile Ala Leu Glu Glu Ala Gly Arg  
485 490 495

Tyr Ala Ala Glu Asp Ala Asp Val Thr Leu Gln Leu His Leu Lys Met  
500 505 510

Trp Pro Asp Leu Gln Lys His Lys Gly Pro Leu Asn Val Phe Glu Asn  
515 520 525

Ile Glu Met Pro Leu Val Pro Val Leu Ser Arg Ile Glu Arg Asn Gly  
530 535 540

Val Lys Ile Asp Pro Lys Val Leu His Asn His Ser Glu Glu Leu Thr  
545 550 555 560

Leu Arg Leu Ala Glu Leu Glu Lys Lys Ala His Glu Ile Ala Gly Glu  
565 570 575

Glu Phe Asn Leu Ser Ser Thr Lys Gln Leu Gln Thr Ile Leu Phe Glu  
580 585 590

Lys Gln Gly Ile Lys Pro Leu Lys Lys Thr Pro Gly Gly Ala Pro Ser  
595 600 605

Thr Ser Glu Glu Val Leu Glu Leu Ala Leu Asp Tyr Pro Leu Pro  
610 615 620

Lys Val Ile Leu Glu Tyr Arg Gly Leu Ala Lys Leu Lys Ser Thr Tyr  
625 630 635 640

Thr Asp Lys Leu Pro Leu Met Ile Asn Pro Lys Thr Gly Arg Val His  
645 650 655

Thr Ser Tyr His Gln Ala Val Thr Ala Thr Gly Arg Leu Ser Ser Thr  
660 665 670

Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Asn Glu Glu Gly Arg Arg  
675 680 685

Ile Arg Gln Ala Phe Ile Ala Pro Glu Asp Tyr Val Ile Val Ser Ala  
690 695 700

Asp Tyr Ser Gln Ile Glu Leu Arg Ile Met Ala His Leu Ser Arg Asp  
705 710 715 720

Lys Gly Leu Leu Thr Ala Phe Ala Glu Gly Lys Asp Ile His Arg Ala  
725 730 735

Thr Ala Ala Glu Val Phe Gly Leu Pro Leu Glu Thr Val Thr Ser Glu  
740 745 750

Gln Arg Arg Ser Ala Lys Ala Ile Asn Phe Gly Leu Ile Tyr Gly Met  
755 760 765

Ser Ala Phe Gly Leu Ala Arg Gln Leu Asn Ile Pro Arg Lys Glu Ala  
770 775 780

Gln Lys Tyr Met Asp Leu Tyr Phe Glu Arg Tyr Pro Gly Val Leu Glu  
785 790 795 800

Tyr Met Glu Arg Thr Arg Ala Gln Ala Lys Glu Gln Gly Tyr Val Glu  
805 810 815

Thr Leu Asp Gly Arg Arg Leu Tyr Leu Pro Asp Ile Lys Ser Ser Asn  
820 825 830

Gly Ala Arg Arg Ala Ala Ala Glu Arg Ala Ala Ile Asn Ala Pro Met  
835 840 845

Gln Gly Thr Ala Ala Asp Ile Ile Lys Arg Ala Met Ile Ala Val Asp  
850 855 860

Ala Trp Leu Gln Ala Glu Gln Pro Arg Val Arg Met Ile Met Gln Val  
865 870 875 880

His Asp Glu Leu Val Phe Glu Val His Lys Asp Asp Val Asp Ala Val  
885 890 895

Ala Lys Gln Ile His Gln Leu Met Glu Asn Cys Thr Arg Leu Asp Val  
900 905 910

Pro Leu Leu Val Glu Val Gly Ser Gly Glu Asn Trp Asp Gln Ala His  
915 920 925

<210> 74  
<211> 893  
<212> PRT  
<213> Thermotoga maritima

<400> 74

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala  
1 5 10 15

Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr  
20 25 30

Asn Ala Thr Tyr Gly Val Ala Arg Met Leu Val Arg Phe Ile Lys Asp  
35 40 45

His Ile Ile Val Gly Lys Asp Tyr Val Ala Val Ala Phe Asp Lys Lys  
50 55 60

Ala Ala Thr Phe Arg His Lys Leu Leu Glu Thr Tyr Lys Ala Gln Arg  
65 70 75 80

Pro Lys Thr Pro Asp Leu Leu Ile Gln Gln Leu Pro Tyr Ile Lys Lys  
85 90 95

Leu Val Glu Ala Leu Gly Met Lys Val Leu Glu Val Glu Gly Tyr Glu  
100 105 110

Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Lys Gly Leu Pro Leu Phe  
115 120 125

Asp Glu Ile Phe Ile Val Thr Gly Asp Lys Asp Met Leu Gln Leu Val  
130 135 140

Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu  
145 150 155 160

Glu Leu Tyr Asp Ala Gln Lys Val Lys Glu Lys Tyr Gly Val Glu Pro  
165 170 175

Gln Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Glu Ile Asp Asn  
180 185 190

Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu  
195 200 205

Glu Lys Tyr Lys Asp Leu Glu Asp Ile Leu Asn His Val Arg Glu Leu  
210 215 220

Pro Gln Lys Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Asn Ala Ile  
225 230 235 240

Leu Ser Lys Lys Leu Ala Ile Leu Glu Thr Asn Val Pro Ile Glu Ile  
245 250 255

Asn Trp Glu Glu Leu Arg Tyr Gln Gly Tyr Asp Arg Glu Lys Leu Leu  
260 265 270

Pro Leu Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln  
275 280 285

Leu Tyr Glu Glu Ser Glu Pro Val Gly Tyr Arg Ile Val Lys Asp Leu  
290 295 300

Val Glu Phe Glu Lys Leu Ile Glu Lys Leu Arg Glu Ser Pro Ser Phe  
305 310 315 320

Ala Ile Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asp Cys Asp Ile  
325 330 335

Val Gly Ile Ser Val Ser Phe Lys Pro Lys Glu Ala Tyr Tyr Ile Pro  
340 345 350

Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Lys Glu Val Leu Lys  
355 360 365

Lys Leu Lys Glu Ile Leu Glu Asp Pro Gly Ala Lys Ile Val Gly Gln  
370 375 380

Asn Leu Lys Phe Asp Tyr Lys Val Leu Met Val Lys Gly Val Glu Pro  
385 390 395 400

Val Pro Pro Tyr Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro  
405 410 415

Asn Glu Lys Lys Phe Asn Leu Asp Asp Leu Ala Leu Lys Phe Leu Gly  
420 425 430

Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Phe Pro Leu  
435 440 445

Phe Gly Phe Ser Phe Ala Asp Val Pro Val Glu Lys Ala Ala Asn Tyr  
450 455 460

Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Thr Leu Ser  
465 470 475 480

Leu Lys Leu His Glu Ala Asp Leu Glu Asn Val Phe Tyr Lys Ile Glu  
485 490 495

Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr  
500 505 510

Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys  
515 520 525

Leu Glu Glu Leu Ala Glu Glu Ile Tyr Arg Ile Ala Gly Glu Pro Phe  
530 535 540

Asn Ile Asn Ser Pro Lys Gln Val Ser Arg Ile Leu Phe Glu Lys Leu  
545 550 555 560

Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Asp Tyr Ser Thr  
565 570 575

Arg Ile Glu Val Leu Glu Leu Ala Gly Glu His Glu Ile Ile Pro  
580 585 590

Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile  
595 600 605

Asp Ala Leu Pro Lys Met Val Asn Pro Lys Thr Gly Arg Ile His Ala  
610 615 620

Ser Phe Asn Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
625 630 635 640

Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile  
645 650 655

Arg Lys Ala Ile Val Pro Gln Asp Pro Asn Trp Trp Ile Val Ser Ala  
660 665 670

Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp  
675 680 685

Glu Asn Leu Leu Arg Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu  
690 695 700

Thr Ala Ser Arg Ile Phe Asn Val Lys Pro Glu Glu Val Thr Glu Glu  
705 710 715 720

Met Arg Arg Ala Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val  
725 730 735

Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Val Pro Val Lys Glu Ala  
740 745 750

Glu Lys Met Ile Val Asn Tyr Phe Val Leu Tyr Pro Lys Val Arg Asp  
755 760 765

Tyr Ile Gln Arg Val Val Ser Glu Ala Lys Glu Lys Gly Tyr Val Arg  
770 775 780

Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp  
785 790 795 800

Arg Asn Thr Gln Ala Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile  
805 810 815

Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Glu Ile Asp  
820 825 830

Arg Glu Leu Lys Glu Arg Lys Met Arg Ser Lys Met Ile Ile Gln Val  
835 840 845

His Asp Glu Leu Val Phe Glu Val Pro Asn Glu Glu Lys Asp Ala Leu  
850 855 860

Val Glu Leu Val Lys Asp Arg Met Thr Asn Val Val Lys Leu Ser Val  
865 870 875 880

Pro Leu Glu Val Asp Val Thr Ile Gly Lys Thr Trp Ser  
885 890

<210> 75  
 <211> 893  
 <212> PRT  
 <213> Thermotoga neapolitana  
 <400> 75

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala	1	5	10	15
Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr	20	25	30	
Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu	35	40	45	
His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys	50	55	60	
Ala Ala Thr Phe Arg His Lys Leu Leu Glu Ala Tyr Lys Ala Gln Arg	65	70	75	80
Pro Lys Thr Pro Asp Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg	85	90	95	
Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu	100	105	110	
Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Lys Gly Cys Thr Phe Phe	115	120	125	
Asp Glu Ile Phe Ile Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val	130	135	140	
Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu	145	150	155	160
Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro	165	170	175	
His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Glu Ile Asp Asn	180	185	190	
Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu	195	200	205	
Gly Lys Tyr Arg Asn Leu Glu Asp Ile Leu Glu His Ala Arg Glu Leu	210	215	220	

Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile  
225 230 235 240

Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val  
245 250 255

Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu  
260 265 270

Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln  
275 280 285

Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His  
290 295 300

Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe  
305 310 315 320

Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile  
325 330 335

Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro  
340 345 350

Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser  
355 360 365

Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln  
370 375 380

Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro  
385 390 395 400

Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro  
405 410 415

Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly  
420 425 430

Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu  
435 440 445

Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr  
450 455 460

Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser  
465 470 475 480

Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu  
485 490 495

Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr  
500 505 510

Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys  
515 520 525

Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe  
530 535 540

Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu  
545 550 555 560

Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Ala Tyr Ser Thr  
565 570 575

Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro  
580 585 590

Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile  
595 600 605

Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala  
610 615 620

Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
625 630 635 640

Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile  
645 650 655

Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala  
660 665 670

Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp  
675 680 685

Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu  
690 695 700

Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu  
705 710 715 720

Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val  
725 730 735

Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala  
740 745 750

Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser  
755 760 765

Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg  
770 775 780

Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp  
785 790 795 800

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile  
805 810 815

Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp  
820 825 830

Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val  
835 840 845

His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu  
850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val  
865 870 875 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser  
885 890